



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 01:15 PM UTC

PDB ID : 3WT1 / pdb_00003wt1
Title : Crystal structure of the b'-a' domain of thermophilic fungal protein disulfide isomerase (reduced form)
Authors : Inagaki, K.; Satoh, T.; Itoh, S.G.; Okumura, H.; Kato, K.
Deposited on : 2014-04-02
Resolution : 1.85 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

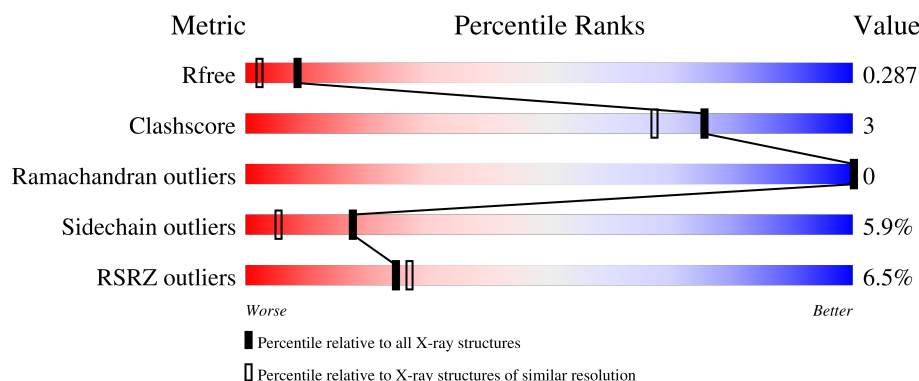
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.85 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	3428 (1.86-1.86)
Clashscore	190562	3579 (1.86-1.86)
Ramachandran outliers	187476	3553 (1.86-1.86)
Sidechain outliers	187428	3553 (1.86-1.86)
RSRZ outliers	180081	3429 (1.86-1.86)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	247	 4% 87% 10% ..
1	B	247	 9% 90% 6% ..
1	C	247	 8% 89% 6% ..
1	D	247	 4% 84% 11% ...

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 7831 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Protein disulfide-isomerase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	244	Total	C	N	O	S	0	2	0
			1901	1227	304	367	3			
1	B	242	Total	C	N	O	S	0	0	0
			1878	1214	299	362	3			
1	C	242	Total	C	N	O	S	0	1	0
			1883	1217	299	364	3			
1	D	242	Total	C	N	O	S	0	1	0
			1883	1217	299	364	3			

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	203	GLY	-	expression tag	UNP P55059
A	204	PRO	-	expression tag	UNP P55059
A	205	LEU	-	expression tag	UNP P55059
A	206	GLY	-	expression tag	UNP P55059
A	207	SER	-	expression tag	UNP P55059
B	203	GLY	-	expression tag	UNP P55059
B	204	PRO	-	expression tag	UNP P55059
B	205	LEU	-	expression tag	UNP P55059
B	206	GLY	-	expression tag	UNP P55059
B	207	SER	-	expression tag	UNP P55059
C	203	GLY	-	expression tag	UNP P55059
C	204	PRO	-	expression tag	UNP P55059
C	205	LEU	-	expression tag	UNP P55059
C	206	GLY	-	expression tag	UNP P55059
C	207	SER	-	expression tag	UNP P55059
D	203	GLY	-	expression tag	UNP P55059
D	204	PRO	-	expression tag	UNP P55059
D	205	LEU	-	expression tag	UNP P55059
D	206	GLY	-	expression tag	UNP P55059
D	207	SER	-	expression tag	UNP P55059

- Molecule 2 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			6	3	3		
2	B	1	Total	C	O	0	0
			6	3	3		
2	C	1	Total	C	O	0	0
			6	3	3		
2	D	1	Total	C	O	0	0
			6	3	3		

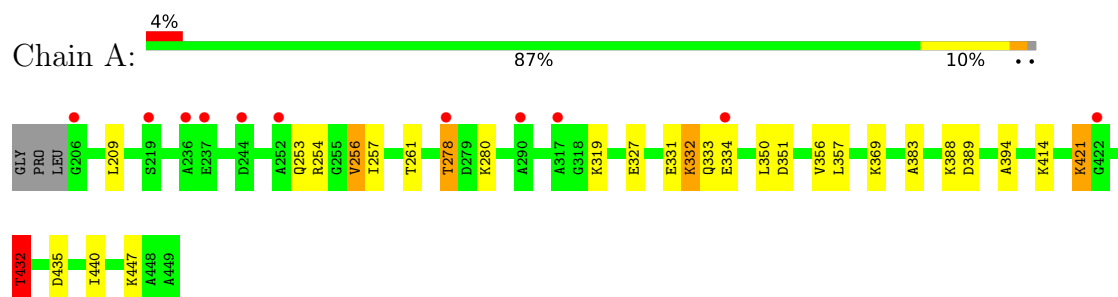
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	75	Total	O	0	0
			75	75		
3	B	45	Total	O	0	0
			45	45		
3	C	79	Total	O	0	0
			79	79		
3	D	63	Total	O	0	0
			63	63		

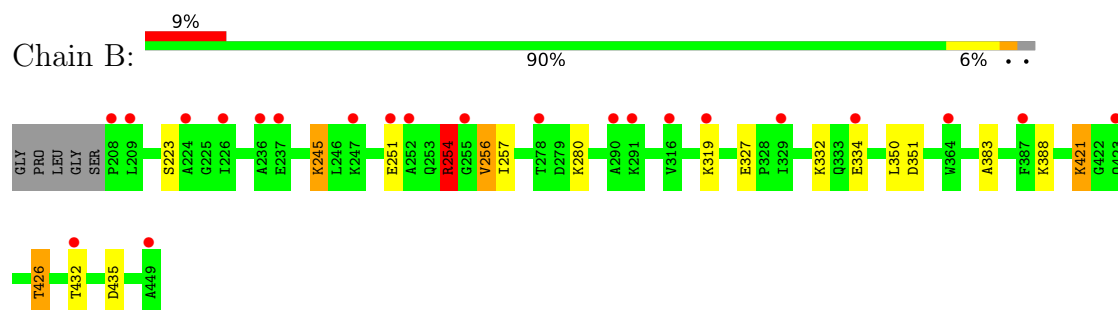
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

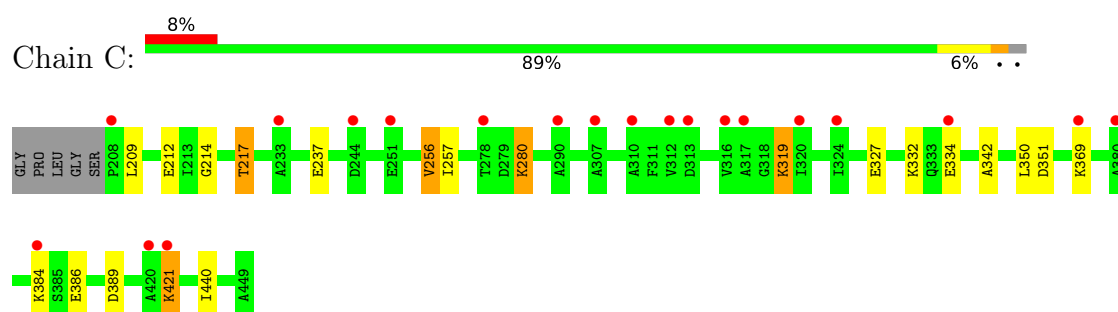
- Molecule 1: Protein disulfide-isomerase



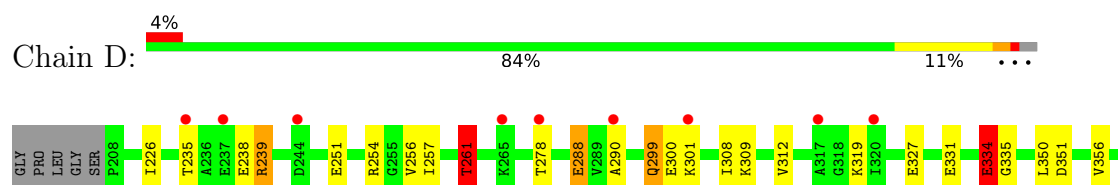
- Molecule 1: Protein disulfide-isomerase



- Molecule 1: Protein disulfide-isomerase



- Molecule 1: Protein disulfide-isomerase





4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	65.77Å 67.75Å 70.25Å 105.92° 113.13° 96.59°	Depositor
Resolution (Å)	20.00 – 1.85 20.00 – 1.85	Depositor EDS
% Data completeness (in resolution range)	92.1 (20.00-1.85) 92.1 (20.00-1.85)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.32 (at 1.85Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, R_{free}	0.238 , 0.278 (Not available) , 0.287	Depositor DCC
R_{free} test set	4080 reflections (4.61%)	wwPDB-VP
Wilson B-factor (Å ²)	28.9	Xtriage
Anisotropy	0.272	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 26.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	7831	wwPDB-VP
Average B, all atoms (Å ²)	41.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.82% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GOL

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	1.06	3/1950 (0.2%)	1.02	4/2641 (0.2%)
1	B	0.88	0/1921	0.95	2/2602 (0.1%)
1	C	0.99	1/1929 (0.1%)	1.01	4/2613 (0.2%)
1	D	0.94	1/1929 (0.1%)	0.99	7/2613 (0.3%)
All	All	0.97	5/7729 (0.1%)	0.99	17/10469 (0.2%)

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	440	ILE	N-CA	-5.94	1.39	1.46
1	C	342	ALA	C-O	-5.57	1.17	1.24
1	A	414	LYS	C-O	5.30	1.30	1.23
1	A	357	LEU	CA-C	-5.17	1.46	1.52
1	D	391	VAL	CA-C	-5.05	1.46	1.52

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	334	GLU	N-CA-C	7.39	119.24	111.03
1	D	299	GLN	CB-CG-CD	6.00	122.80	112.60
1	C	209	LEU	N-CA-CB	5.84	118.66	110.07
1	C	440	ILE	N-CA-C	5.63	116.36	110.62
1	B	327	GLU	N-CA-C	-5.59	102.15	110.20
1	A	432	THR	N-CA-CB	-5.57	101.83	110.29
1	B	254	ARG	N-CA-CB	5.50	118.44	109.69
1	D	299	GLN	CG-CD-NE2	5.46	124.59	116.40
1	A	356	VAL	N-CA-C	5.38	115.34	107.37
1	C	327	GLU	N-CA-C	-5.35	102.50	110.20
1	A	327	GLU	N-CA-C	-5.25	102.64	110.20
1	D	239	ARG	CG-CD-NE	5.24	123.52	112.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	261	THR	N-CA-CB	-5.22	102.13	110.63
1	D	356	VAL	N-CA-C	5.17	115.02	107.37
1	A	394	ALA	N-CA-C	5.10	116.93	109.24
1	C	217	THR	N-CA-CB	-5.09	103.60	110.67
1	D	327	GLU	N-CA-C	-5.05	102.92	110.20

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1901	0	1896	14	0
1	B	1878	0	1872	10	0
1	C	1883	0	1876	9	0
1	D	1883	0	1876	15	0
2	A	6	0	8	0	0
2	B	6	0	8	0	0
2	C	6	0	8	0	0
2	D	6	0	8	0	0
3	A	75	0	0	2	0
3	B	45	0	0	1	0
3	C	79	0	0	0	0
3	D	63	0	0	1	0
All	All	7831	0	7552	46	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 3.

All (46) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:212:GLU:O	1:C:217:THR:HG21	1.53	1.07
1:B:432:THR:HG23	1:B:435:ASP:H	1.48	0.78
1:C:280:LYS:HA	1:C:280:LYS:HE2	1.72	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:235:THR:HG23	1:D:238:GLU:H	1.59	0.68
1:B:383:ALA:O	1:B:388:LYS:HG3	1.94	0.67
1:D:447:LYS:NZ	3:D:629:HOH:O	2.28	0.66
1:D:239:ARG:HD2	1:D:261:THR:HG23	1.79	0.64
1:C:319:LYS:O	1:C:319:LYS:HD2	1.99	0.62
1:B:426:THR:HG23	3:B:640:HOH:O	1.99	0.62
1:D:251:GLU:OE2	1:D:254:ARG:NH1	2.32	0.60
1:A:383:ALA:O	1:A:388:LYS:HG3	2.05	0.56
1:C:214:GLY:H	1:C:217:THR:HG22	1.71	0.55
1:B:223:SER:HB3	1:D:226:ILE:HG22	1.90	0.54
1:A:432:THR:HG22	1:A:435:ASP:CB	2.39	0.53
1:A:432:THR:CG2	1:A:435:ASP:H	2.23	0.52
1:A:278:THR:HA	3:A:661:HOH:O	2.10	0.52
1:A:331:GLU:HG2	1:A:332:LYS:HG3	1.92	0.51
1:B:251:GLU:O	1:B:254:ARG:HG2	2.10	0.51
1:C:386:GLU:CD	1:C:386:GLU:H	2.20	0.50
1:A:432:THR:HG22	1:A:435:ASP:HB2	1.92	0.49
1:C:350:LEU:HA	1:C:421:LYS:HG2	1.96	0.48
1:A:331:GLU:HG2	1:A:332:LYS:CD	2.44	0.47
1:B:350:LEU:HA	1:B:421:LYS:HG2	1.96	0.47
1:A:350:LEU:HA	1:A:421:LYS:HG2	1.96	0.47
1:D:334:GLU:HG3	1:D:335:GLY:N	2.30	0.46
1:C:256:VAL:HG22	1:C:257:ILE:HG13	1.97	0.46
1:C:351:ASP:OD1	1:C:351:ASP:C	2.58	0.46
1:D:350:LEU:HA	1:D:421:LYS:HG2	1.98	0.46
1:A:432:THR:HG22	1:A:435:ASP:H	1.81	0.46
1:B:256:VAL:HG22	1:B:257:ILE:HG13	1.98	0.45
1:D:256:VAL:HG12	1:D:257:ILE:HG13	1.98	0.45
1:A:256:VAL:HG22	1:A:257:ILE:HG13	1.98	0.45
1:D:308:ILE:O	1:D:312:VAL:HG12	2.16	0.45
1:D:239:ARG:HD2	1:D:261:THR:CG2	2.45	0.45
1:B:351:ASP:OD1	1:B:351:ASP:C	2.60	0.44
1:A:351:ASP:OD1	1:A:351:ASP:C	2.60	0.44
1:D:385:SER:O	1:D:388:LYS:HD2	2.19	0.43
1:B:223:SER:CB	1:D:226:ILE:HG22	2.47	0.42
1:D:309:LYS:HA	1:D:312:VAL:HG12	1.99	0.42
1:A:447:LYS:HE3	3:A:674:HOH:O	2.18	0.42
1:D:288:GLU:HG3	1:D:290:ALA:O	2.20	0.42
1:A:331:GLU:HG2	1:A:332:LYS:HD3	2.03	0.41
1:C:214:GLY:H	1:C:217:THR:CG2	2.31	0.41
1:B:245:LYS:HA	1:B:245:LYS:HD3	1.91	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:351:ASP:C	1:D:351:ASP:OD1	2.63	0.40
1:A:253:GLN:O	1:A:254:ARG:C	2.65	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	244/247 (99%)	241 (99%)	3 (1%)	0	100	100
1	B	240/247 (97%)	237 (99%)	3 (1%)	0	100	100
1	C	241/247 (98%)	238 (99%)	3 (1%)	0	100	100
1	D	241/247 (98%)	236 (98%)	5 (2%)	0	100	100
All	All	966/988 (98%)	952 (99%)	14 (1%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	199/199 (100%)	185 (93%)	14 (7%)	14	3
1	B	196/199 (98%)	187 (95%)	9 (5%)	24	9
1	C	197/199 (99%)	186 (94%)	11 (6%)	19	6

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	D	197/199 (99%)	182 (92%)	15 (8%)	12	3
All	All	789/796 (99%)	740 (94%)	49 (6%)	18	5

All (49) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	209	LEU
1	A	256	VAL
1	A	261	THR
1	A	278	THR
1	A	280	LYS
1	A	319	LYS
1	A	332	LYS
1	A	333	GLN
1	A	334	GLU
1	A	369	LYS
1	A	389[A]	ASP
1	A	389[B]	ASP
1	A	421	LYS
1	A	432	THR
1	B	245	LYS
1	B	254	ARG
1	B	256	VAL
1	B	280	LYS
1	B	319	LYS
1	B	332	LYS
1	B	334	GLU
1	B	421	LYS
1	B	426	THR
1	C	237	GLU
1	C	256	VAL
1	C	280	LYS
1	C	319	LYS
1	C	332	LYS
1	C	334	GLU
1	C	369	LYS
1	C	384	LYS
1	C	389[A]	ASP
1	C	389[B]	ASP
1	C	421	LYS
1	D	261	THR
1	D	278	THR

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Mol	Chain	Res	Type
1	D	288	GLU
1	D	299	GLN
1	D	300	GLU
1	D	301	LYS
1	D	319	LYS
1	D	331	GLU
1	D	334	GLU
1	D	384	LYS
1	D	388	LYS
1	D	389[A]	ASP
1	D	389[B]	ASP
1	D	408	GLN
1	D	421	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	273	ASN
1	A	292	ASN
1	B	292	ASN
1	B	293	GLN
1	C	292	ASN
1	D	253	GLN
1	D	258	ASN
1	D	273	ASN
1	D	408	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

4 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	GOL	B	501	-	5,5,5	1.11	0	5,5,5	1.34	0
2	GOL	A	501	-	5,5,5	1.12	0	5,5,5	1.30	1 (20%)
2	GOL	C	501	-	5,5,5	1.13	0	5,5,5	1.71	2 (40%)
2	GOL	D	501	-	5,5,5	1.25	0	5,5,5	1.37	1 (20%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	GOL	B	501	-	-	2/4/4/4	-
2	GOL	A	501	-	-	3/4/4/4	-
2	GOL	C	501	-	-	2/4/4/4	-
2	GOL	D	501	-	-	2/4/4/4	-

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	501	GOL	O1-C1-C2	2.27	120.62	110.38
2	C	501	GOL	C3-C2-C1	2.24	120.01	111.80
2	D	501	GOL	O3-C3-C2	2.21	120.34	110.38
2	A	501	GOL	C3-C2-C1	2.02	119.19	111.80

There are no chirality outliers.

All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	501	GOL	O1-C1-C2-O2
2	C	501	GOL	O1-C1-C2-O2
2	A	501	GOL	C1-C2-C3-O3
2	B	501	GOL	O1-C1-C2-C3
2	C	501	GOL	O1-C1-C2-C3
2	D	501	GOL	O1-C1-C2-C3
2	D	501	GOL	O1-C1-C2-O2
2	A	501	GOL	O1-C1-C2-O2
2	A	501	GOL	O2-C2-C3-O3

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	244/247 (98%)	0.56	11 (4%) 38 41	17, 35, 60, 82	2 (0%)
1	B	242/247 (97%)	0.92	22 (9%) 15 15	28, 42, 65, 87	0
1	C	242/247 (97%)	0.72	20 (8%) 17 18	16, 37, 65, 88	1 (0%)
1	D	242/247 (97%)	0.75	10 (4%) 41 45	19, 40, 62, 80	1 (0%)
All	All	970/988 (98%)	0.74	63 (6%) 25 27	16, 39, 63, 88	4 (0%)

All (63) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	252	ALA	4.2
1	C	208	PRO	3.7
1	C	310	ALA	3.5
1	D	290	ALA	3.3
1	B	329	ILE	3.3
1	C	316	VAL	3.2
1	C	278	THR	3.1
1	B	423	GLN	3.1
1	B	290	ALA	3.1
1	B	208	PRO	3.0
1	A	334	GLU	3.0
1	B	247	LYS	2.9
1	B	319	LYS	2.9
1	C	384	LYS	2.9
1	C	233	ALA	2.8
1	C	251	GLU	2.8
1	C	244	ASP	2.8
1	B	209	LEU	2.8
1	C	320	ILE	2.8
1	D	235	THR	2.7
1	D	278	THR	2.7

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Mol	Chain	Res	Type	RSRZ
1	D	265	LYS	2.7
1	B	224	ALA	2.6
1	B	334	GLU	2.6
1	C	317	ALA	2.6
1	D	317	ALA	2.6
1	B	278	THR	2.6
1	C	334	GLU	2.6
1	A	236	ALA	2.6
1	A	290	ALA	2.5
1	C	307	ALA	2.5
1	B	291	LYS	2.5
1	C	420	ALA	2.5
1	B	237	GLU	2.5
1	B	364	TRP	2.4
1	A	422	GLY	2.4
1	B	316	VAL	2.4
1	A	278	THR	2.3
1	B	226	ILE	2.3
1	D	320	ILE	2.3
1	B	236	ALA	2.3
1	B	449	ALA	2.3
1	C	324	ILE	2.3
1	A	219	SER	2.3
1	D	237	GLU	2.3
1	A	252	ALA	2.2
1	A	317	ALA	2.2
1	B	432	THR	2.2
1	B	387	PHE	2.2
1	A	206	GLY	2.2
1	C	290	ALA	2.2
1	D	301	LYS	2.2
1	A	237	GLU	2.1
1	D	420	ALA	2.1
1	A	244	ASP	2.1
1	D	244	ASP	2.1
1	B	251	GLU	2.1
1	C	369	LYS	2.1
1	B	255	GLY	2.1
1	C	312	VAL	2.1
1	C	380	ALA	2.1
1	C	313	ASP	2.1
1	C	421	LYS	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	GOL	C	501	6/6	0.75	0.12	33,36,40,42	0
2	GOL	A	501	6/6	0.79	0.16	33,40,53,54	0
2	GOL	D	501	6/6	0.81	0.12	35,38,40,45	0
2	GOL	B	501	6/6	0.89	0.10	45,48,50,58	0

6.5 Other polymers [i](#)

There are no such residues in this entry.